

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/526,429
Source: PGT/10
Date Processed by STIC: 3/11/05

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PCT

RAW SEQUENCE LISTING

DATE: 03/11/2005

PATENT APPLICATION: US/10/526,429

TIME: 09:34:34

Input Set : D:\Sequence Listing.txt

Output Set: N:\CRF4\03112005\J526429.raw

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5 <110> APPLICANT: THE HOSPITAL FOR SICK CHILDREN
9 <120> TITLE OF INVENTION: DIAGNOSIS OF SHWACHMAN-DIAMOND SYNDROME
13 <130> FILE REFERENCE: 3206-264/PAR
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/526,429
C--> 19 <141> CURRENT FILING DATE: 2005-02-28
23 <150> PRIOR APPLICATION NUMBER: 60/406,950
25 <151> PRIOR FILING DATE: 2002-08-30
29 <160> NUMBER OF SEQ ID NOS: 50
33 <170> SOFTWARE: PatentIn version 3.1
37 <210> SEQ ID NO: 1
39 <211> LENGTH: 1604
41 <212> TYPE: DNA
43 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
49 <221> NAME/KEY: misc_feature
51 <223> OTHER INFORMATION: human SBDS
55 <220> FEATURE:
57 <221> NAME/KEY: CDS
59 <222> LOCATION: (185)..(934)
61 <223> OTHER INFORMATION:
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66 gtaagtaagc ctgccagaca cactgtgacg gctgcctgaa gctagtgagt cgcggcgccg      60
68 cgcactggtg gttgggtcag tgccgcgcgc cgatcggtcg ttaccgcgag gcgctggtgg      120
70 ccttcaggct ggacggcgcg ggtcagccct ggttcgcggg cttctgggtc tttgaacagc      180
72 cgcg atg tcg atc ttc acc ccc acc aac cag atc cgc cta acc aat gtg      229
73 Met Ser Ile Phe Thr Pro Thr Asn Gln Ile Arg Leu Thr Asn Val
74 1 5 10 15
76 gcc gtg gta cgg atg aag cgt gcc ggg aag cgc ttc gaa atc gcc tgc      277
77 Ala Val Val Arg Met Lys Arg Ala Gly Lys Arg Phe Glu Ile Ala Cys
78 20 25 30
80 tac aaa aac aag gtc gtc ggc tgg cgg agc ggc gtg gaa aaa gac .ctc      325
81 Tyr Lys Asn Lys Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp Leu
82 35 40 45
84 gat gaa gtt ctg cag acc cac tca gtg ttt gta aat gtt tct aaa ggt      373
85 Asp Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys Gly
86 50 55 60
88 cag gtt gcc aaa aag gaa gat ctc atc agt gcg ttt gga aca gat gac      421
89 Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp Asp
90 65 70 75
92 caa act gaa atc tgt aag cag att ttg act aaa gga gaa gtt caa gta      469
93 Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln Val
94 80 85 90 95
96 tca gat aaa gaa aga cac aca caa ctg gag cag atg ttt agg gac att      517

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97 Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp Ile
98                               100                               105                               110
100 gca act att gtg gca gac aaa tgt gtg aat cct gaa aca aag aga cca      565
101 Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg Pro
102                               115                               120                               125
104 tac acc gtg atc ctt att gag aga gcc atg aag gac atc cac tat tcg      613
105 Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr Ser
106                               130                               135                               140
108 gtg aaa acc aac aag agt aca aaa cag cag gct ttg gaa gtg ata aag      661
109 Val Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile Lys
110                               145                               150                               155
112 cag tta aaa gag aaa atg aag ata gaa cgt gct cac atg agg ctt cgg      709
113 Gln Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Arg Leu Arg
114 160                               165                               170                               175
116 ttc atc ctt cca gtc aat gaa ggc aag aag ctg aaa gaa aag ctc aag      757
117 Phe Ile Leu Pro Val Asn Glu Gly Lys Lys Leu Lys Glu Lys Leu Lys
118                               180                               185                               190
120 cca ctg atc aag gtc ata gaa agt gaa gat tat ggc caa cag tta gaa      805
121 Pro Leu Ile Lys Val Ile Glu Ser Glu Asp Tyr Gly Gln Gln Leu Glu
122                               195                               200                               205
124 atc gta tgt ctg att gac ccg ggc tgc ttc cga gaa att gat gag cta      853
125 Ile Val Cys Leu Ile Asp Pro Gly Cys Phe Arg Glu Ile Asp Glu Leu
126                               210                               215                               220
128 ata aaa aag gaa act aaa ggc aaa ggt tct ttg gaa gta ctc aat ctg      901
129 Ile Lys Lys Glu Thr Lys Gly Lys Gly Ser Leu Glu Val Leu Asn Leu
130                               225                               230                               235
132 aaa gat gta gaa gaa gga gat gag aaa ttt gaa tgacacccat caatctcttc      954
133 Lys Asp Val Glu Glu Gly Asp Glu Lys Phe Glu
134 240                               245                               250
136 acctctaaaa cactaaagtgt tttccgtttc cgacggcact gtttcatgtc tgtgggtctgc      1014
138 caaatacttg cttaaactat ttgacatttt ctactttgtg ttaacagtgg acacagcaag      1074
140 gcttttctac ataagtataa taatgtggga atgatttggg ttttaattata aactgggggtc      1134
142 taaatcctaa agcaaaattg aaactccaag atgcaaagtc cagagtggca ttttgctact      1194
144 ctgtctcatg ccttgatagc tttccaaaat gaaagttact tgaggcagct cttgtgggtg      1254
146 aaaagttatt tgtacagtag agtaagatta ttaggggtat gtctatacaa caaaaggggg      1314
148 ggtctttcct aaaaaagaaa acatatgatg cttcatttct acttaatgga acttgtgttc      1374
150 tgagggtcat tatggtatcg taatgtaaag cttggatgat gttcctgatt atctgagaaa      1434
152 cagatataga aaaattgtgc cggacttacc tttcattgaa catgctgcca taacttagat      1494
154 tattcttggt taaaaataa aagtcactta tttctaattc ttaaagttta taatatatat      1554
156 taatatagct aaaattgtat gtaatcaata aaaccactct tatgtttatt      1604
159 <210> SEQ ID NO: 2
161 <211> LENGTH: 250
163 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
169 <220> FEATURE:
171 <221> NAME/KEY: misc_feature
173 <223> OTHER INFORMATION: human SBDS
175 <400> SEQUENCE: 2
177 Met Ser Ile Phe Thr Pro Thr Asn Gln Ile Arg Leu Thr Asn Val Ala

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178 1          5          10          15
181 Val Val Arg Met Lys Arg Ala Gly Lys Arg Phe Glu Ile Ala Cys Tyr
182          20          25          30
185 Lys Asn Lys Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp Leu Asp
186          35          40          45
189 Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys Gly Gln
190          50          55          60
193 Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp Asp Gln
194 65          70          75          80
197 Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln Val Ser
198          85          90          95
201 Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp Ile Ala
202          100          105          110
205 Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg Pro Tyr
206          115          120          125
209 Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr Ser Val
210          130          135          140
213 Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile Lys Gln
214 145          150          155          160
217 Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Arg Leu Arg Phe
218          165          170          175
221 Ile Leu Pro Val Asn Glu Gly Lys Lys Leu Lys Glu Lys Leu Lys Pro
222          180          185          190
225 Leu Ile Lys Val Ile Glu Ser Glu Asp Tyr Gly Gln Gln Leu Glu Ile
226          195          200          205
229 Val Cys Leu Ile Asp Pro Gly Cys Phe Arg Glu Ile Asp Glu Leu Ile
230          210          215          220
233 Lys Lys Glu Thr Lys Gly Lys Gly Ser Leu Glu Val Leu Asn Leu Lys
234 225          230          235          240
237 Asp Val Glu Glu Gly Asp Glu Lys Phe Glu
238          245          250
241 <210> SEQ ID NO: 3
243 <211> LENGTH: 250
245 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
251 <220> FEATURE:
253 <221> NAME/KEY: misc_feature
255 <223> OTHER INFORMATION: human SBDS
259 <400> SEQUENCE: 3
261 Met Ser Ile Phe Thr Pro Thr Asn Gln Ile Arg Leu Thr Asn Val Ala
262 1          5          10          15
265 Val Val Arg Met Lys Arg Ala Gly Lys Arg Phe Glu Ile Ala Cys Tyr
266          20          25          30
269 Lys Asn Lys Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp Leu Asp
270          35          40          45
273 Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys Gly Gln
274          50          55          60
277 Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp Asp Gln
278 65          70          75          80

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281 Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln Val Ser
282                85                      90                      95
285 Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp Ile Ala
286                100                    105                    110
289 Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg Pro Tyr
290                115                    120                    125
293 Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr Ser Val
294                130                    135                    140
297 Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile Lys Gln
298 145                150                    155                    160
301 Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Arg Leu Arg Phe
302                165                    170                    175
305 Ile Leu Pro Val Asn Glu Gly Lys Lys Leu Lys Glu Lys Leu Lys Pro
306                180                    185                    190
309 Leu Ile Lys Val Ile Glu Ser Glu Asp Tyr Gly Gln Gln Leu Glu Ile
310                195                    200                    205
313 Val Cys Leu Ile Asp Pro Gly Cys Phe Arg Glu Ile Asp Glu Leu Ile
314                210                    215                    220
317 Lys Lys Glu Thr Lys Gly Lys Gly Ser Leu Glu Val Leu Asn Leu Lys
318 225                230                    235                    240
321 Asp Val Glu Glu Gly Asp Glu Lys Phe Glu
322                245                    250
325 <210> SEQ ID NO: 4
327 <211> LENGTH: 19
329 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
337 <223> OTHER INFORMATION: primer
339 <400> SEQUENCE: 4
340 gcgtaaaaag ccacaatac                                     19
343 <210> SEQ ID NO: 5
345 <211> LENGTH: 25
347 <212> TYPE: DNA
349 <213> ORGANISM: Artificial Sequence
353 <220> FEATURE:
355 <223> OTHER INFORMATION: primer
357 <400> SEQUENCE: 5
358 ctatgacagt attcgtaaga ctagg                               25
361 <210> SEQ ID NO: 6
363 <211> LENGTH: 19
365 <212> TYPE: DNA
367 <213> ORGANISM: Artificial Sequence
371 <220> FEATURE:
373 <223> OTHER INFORMATION: primer
375 <400> SEQUENCE: 6
376 ggggatttgt tgtgtcttg                                     19
379 <210> SEQ ID NO: 7
381 <211> LENGTH: 20
383 <212> TYPE: DNA

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385 <213> ORGANISM: Artificial Sequence
389 <220> FEATURE:
391 <223> OTHER INFORMATION: primer
393 <400> SEQUENCE: 7
394 ctttcctcca gaaaaacagc 20
397 <210> SEQ ID NO: 8
399 <211> LENGTH: 20
401 <212> TYPE: DNA
403 <213> ORGANISM: Artificial Sequence
407 <220> FEATURE:
409 <223> OTHER INFORMATION: primer
411 <400> SEQUENCE: 8
412 aaatggtaag gcaaatacgg 20
415 <210> SEQ ID NO: 9
417 <211> LENGTH: 27
419 <212> TYPE: DNA
421 <213> ORGANISM: Artificial Sequence
425 <220> FEATURE:
427 <223> OTHER INFORMATION: primer
429 <400> SEQUENCE: 9
430 accaagttct ttattattag aagtgac 27
433 <210> SEQ ID NO: 10
435 <211> LENGTH: 25
437 <212> TYPE: DNA
439 <213> ORGANISM: Artificial Sequence
443 <220> FEATURE:
445 <223> OTHER INFORMATION: primer
447 <400> SEQUENCE: 10
448 gctcaaacca ttacttacat attga 25
451 <210> SEQ ID NO: 11
453 <211> LENGTH: 18
455 <212> TYPE: DNA
457 <213> ORGANISM: Artificial Sequence
461 <220> FEATURE:
463 <223> OTHER INFORMATION: primer
465 <400> SEQUENCE: 11
466 cacttgcttc catgcaga 18
469 <210> SEQ ID NO: 12
471 <211> LENGTH: 21
473 <212> TYPE: DNA
475 <213> ORGANISM: Artificial Sequence
479 <220> FEATURE:
481 <223> OTHER INFORMATION: primer
483 <400> SEQUENCE: 12
484 aaagggtcat tttaacactt c 21
487 <210> SEQ ID NO: 13
489 <211> LENGTH: 23
491 <212> TYPE: DNA
493 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/526,429

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L:17 M:270 C: Current Application Number differs, Replaced Current Application Number

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:65 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:61